SEQUENCE LISTING

<110> Kazuko, SHINOZAKI
Mie, KASUGA

<120> Environmental Stress-Tolerant Plants

<130> 382.1029DIV2

<150> JP292348/1998
US 09/301,217

<151> 1998-10-14
1999-04-28

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<170> PatentIn Ver. 2.0

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atg aac tca ttt tct gct ttt tct gaa atg ttt ggc tcc gat tac gag 166
Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu
1 5 10 15
tct tcg gtt tcc tca ggc ggt gat tat att ccg acg ctt gcg agc agc 214
Ser Ser Val Ser Ser Gly Gly Asp Tyr Ile Pro Thr Leu Ala Ser Ser
20 25 30
tgc ccc aag aaa ccg gcg ggt cgt aag aag ttt cgt gag act cgt cac 262
Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His
35 40 45
cca ata tac aga gga gtt cgt cgg aga aac tcc ggt aag tgg gtt tgt 310
Pro Ile Tyr Arg Gly Val Arg Arg Arg Asn Ser Gly Lys Trp Val Cys
50 55 60
gag gtt aga gaa cca aac aag aaa aca agg att tgg ctc gga aca ttt 358
Glu Val Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe
65 70 75 80
caa acc gct gag atg gca gct cga gct cac gac gtt gcc gct tta gcc 406
Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala
85 90 95
ctt cgt ggc cga tca gcc tgt ctc aat ttc gct gac tcg gct tgg aga 454
Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg
100 105 110
ctc cga atc ccg gaa tca act tgc gct aag gac atc caa aag gcg gcg 502
Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala
115 120 125
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Ala Glu Ala Ala Leu Ala Phe Gln Asp Glu Met Cys Asp Ala Thr Thr

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gcg gaa cag agc gaa aat gcg ttt tat atg cac gat gag gcg atg ttt   646
Ala Glu Gln Ser Glu Asn Ala Phe Tyr Met His Asp Glu Ala Met Phe
                165                 170                 175
gag atg ccg agt ttg ttg gct aat atg gca gaa ggg atg ctt ttg ccg   694
Glu Met Pro Ser Leu Leu Ala Asn Met Ala Glu Gly Met Leu Leu Pro
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ctt ccg tcc gta cag tgg aat cat aat cat gaa gtc gac ggc gat gat   742
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gac gac gta tcg tta tgg agt tat taaaactcag attattattt ccatttttag  796
Asp Asp Val Ser Leu Trp Ser Tyr
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         35                  40                  45
Pro Ile Tyr Arg Gly Val Arg Arg Arg Asn Ser Gly Lys Trp Val Cys
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Glu Val Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe
 65                  70                  75                  80
Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala
                 85                  90                  95
Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg
            100                 105                 110
Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala
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Ala Glu Ala Ala Leu Ala Phe Gln Asp Glu Met Cys Asp Ala Thr Thr
    130                 135                 140
Asp His Gly Phe Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr Thr
145                 150                 155                 160
Ala Glu Gln Ser Glu Asn Ala Phe Tyr Met His Asp Glu Ala Met Phe
                165                 170                 175
Glu Met Pro Ser Leu Leu Ala Asn Met Ala Glu Gly Met Leu Leu Pro
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ttttcaaatt tcgtccccta tagattgtgt tgtttctggg aaggag atg gca gtt 175
Met Ala Val
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tat gat cag agt gga gat aga aac aga aca caa att gat aca tcg agg 223
Tyr Asp Gln Ser Gly Asp Arg Asn Arg Thr Gln Ile Asp Thr Ser Arg
5 10 15

aaa agg aaa tct aga agt aga ggt gac ggt act act gtg gct gag aga 271
Lys Arg Lys Ser Arg Ser Arg Gly Asp Gly Thr Thr Val Ala Glu Arg
20 25 30 35

tta aag aga tgg aaa gag tat aac gag acc gta gaa gaa gtt tct acc 319
Leu Lys Arg Trp Lys Glu Tyr Asn Glu Thr Val Glu Glu Val Ser Thr
40 45 50

aag aag agg aaa gta cct gcg aaa ggg tcg aag aag ggt tgt atg aaa 367
Lys Lys Arg Lys Val Pro Ala Lys Gly Ser Lys Lys Gly Cys Met Lys
55 60 65

ggt aaa gga gga cca gag aat agc cga tgt agt ttc aga gga gtt agg 415
Gly Lys Gly Gly Pro Glu Asn Ser Arg Cys Ser Phe Arg Gly Val Arg
70 75 80

caa agg att tgg ggt aaa tgg gtt gct gag atc aga gag cct aat cga 463
Gln Arg Ile Trp Gly Lys Trp Val Ala Glu Ile Arg Glu Pro Asn Arg
85 90 95

ggt agc agg ctt tgg ctt ggt act ttc cct act gct caa gaa gct gct 511
Gly Ser Arg Leu Trp Leu Gly Thr Phe Pro Thr Ala Gln Glu Ala Ala
100 105 110 115

tct gct tat gat gag gct gct aaa gct atg tat ggt cct ttg gct cgt 559
Ser Ala Tyr Asp Glu Ala Ala Lys Ala Met Tyr Gly Pro Leu Ala Arg
120 125 130

ctt aat ttc cct cgg tct gat gcg tct gag gtt acg agt acc tca agt 607
Leu Asn Phe Pro Arg Ser Asp Ala Ser Glu Val Thr Ser Thr Ser Ser
135 140 145

cag tct gag gtg tgt act gtt gag act cct ggt tgt gtt cat gtg aaa 655
Gln Ser Glu Val Cys Thr Val Glu Thr Pro Gly Cys Val His Val Lys
150 155 160

aca gag gat cca gat tgt gaa tct aaa ccc ttc tcc ggt gga gtg gag 703
Thr Glu Asp Pro Asp Cys Glu Ser Lys Pro Phe Ser Gly Gly Val Glu
165 170 175

ccg atg tat tgt ctg gag aat ggt gcg gaa gag atg aag aga ggt gtt 751
Pro Met Tyr Cys Leu Glu Asn Gly Ala Glu Glu Met Lys Arg Gly Val
180 185 190 195

aaa gcg gat aag cat tgg ctg agc gag ttt gaa cat aac tat tgg agt 799
Lys Ala Asp Lys His Trp Leu Ser Glu Phe Glu His Asn Tyr Trp Ser
200 205 210

gat att ctg aaa gag aaa gag aaa cag aag gag caa ggg att gta gaa 847
Asp Ile Leu Lys Glu Lys Glu Lys Gln Lys Glu Gln Gly Ile Val Glu
215 220 225

acc tgt cag caa caa cag cag gat tcg cta tct gtt gca gac tat ggt 895
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    245                 250                 255
gat gtc gat gag ctt cta cgt gac cta aat ggc gac gat gtg ttt gca   991
Asp Val Asp Glu Leu Leu Arg Asp Leu Asn Gly Asp Asp Val Phe Ala
260                 265                 270                 275
ggc tta aat cag gac cgg tac ccg ggg aac agt gtt gcc aac ggt tca   1039
Gly Leu Asn Gln Asp Arg Tyr Pro Gly Asn Ser Val Ala Asn Gly Ser
                280                 285                 290
tac agg ccc gag agt caa caa agt ggt ttt gat ccg cta caa agc ctc   1087
Tyr Arg Pro Glu Ser Gln Gln Ser Gly Phe Asp Pro Leu Gln Ser Leu
            295                 300                 305
aac tac gga ata cct ccg ttt cag ctc gag gga aag gat ggt aat gga   1135
Asn Tyr Gly Ile Pro Pro Phe Gln Leu Glu Gly Lys Asp Gly Asn Gly
        310                 315                 320
ttc ttc gac gac ttg agt tac ttg gat ctg gag aac taaacaaaac        1181
Phe Phe Asp Asp Leu Ser Tyr Leu Asp Leu Glu Asn
    325                 330                 335
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tccgagtttt agtgatatag agaactacag aacacgtttt ttcttgttat aaaggtgaac 1301
tgtatatatc gaaacagtga tatgacaata gagaagacaa ctatagtttg ttagtctgct 1361
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         35                  40                  45
Val Ser Thr Lys Lys Arg Lys Val Pro Ala Lys Gly Ser Lys Lys Gly
     50                  55                  60
Cys Met Lys Gly Lys Gly Gly Pro Glu Asn Ser Arg Cys Ser Phe Arg
 65                  70                  75                  80
Gly Val Arg Gln Arg Ile Trp Gly Lys Trp Val Ala Glu Ile Arg Glu
                 85                  90                  95
Pro Asn Arg Gly Ser Arg Leu Trp Leu Gly Thr Phe Pro Thr Ala Gln
            100                 105                 110
Glu Ala Ala Ser Ala Tyr Asp Glu Ala Ala Lys Ala Met Tyr Gly Pro
        115                 120                 125
Leu Ala Arg Leu Asn Phe Pro Arg Ser Asp Ala Ser Glu Val Thr Ser
    130                 135                 140
Thr Ser Ser Gln Ser Glu Val Cys Thr Val Glu Thr Pro Gly Cys Val
145                 150                 155                 160
His Val Lys Thr Glu Asp Pro Asp Cys Glu Ser Lys Pro Phe Ser Gly
                165                 170                 175
Gly Val Glu Pro Met Tyr Cys Leu Glu Asn Gly Ala Glu Glu Met Lys
            180                 185                 190
Arg Gly Val Lys Ala Asp Lys His Trp Leu Ser Glu Phe Glu His Asn
        195                 200                 205
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Tyr Trp Ser Asp Ile Leu Lys Glu Lys Glu Lys Gln Lys Glu Gln Gly
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Ile Val Glu Thr Cys Gln Gln Gln Gln Gln Asp Ser Leu Ser Val Ala
225                 230                 235                 240
Asp Tyr Gly Trp Pro Asn Asp Val Asp Gln Ser His Leu Asp Ser Ser
                245                 250                 255
Asp Met Phe Asp Val Asp Glu Leu Leu Arg Asp Leu Asn Gly Asp Asp
            260                 265                 270
Val Phe Ala Gly Leu Asn Gln Asp Arg Tyr Pro Gly Asn Ser Val Ala
        275                 280                 285
Asn Gly Ser Tyr Arg Pro Glu Ser Gln Gln Ser Gly Phe Asp Pro Leu
    290                 295                 300
Gln Ser Leu Asn Tyr Gly Ile Pro Pro Phe Gln Leu Glu Gly Lys Asp
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acttaaacct tatccagttt cttgaaacag agtactctga tca atg aac tca ttt   175
                                              Met Asn Ser Phe
                                                1
tca gct ttt tct gaa atg ttt ggc tcc gat tac gag cct caa ggc gga   223
Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu Pro Gln Gly Gly
  5                 10                  15                  20
gat tat tgt ccg acg ttg gcc acg agt tgt ccg aag aaa ccg gcg ggc   271
Asp Tyr Cys Pro Thr Leu Ala Thr Ser Cys Pro Lys Lys Pro Ala Gly
                25                  30                  35
cgt aag aag ttt cgt gag act cgt cac cca att tac aga gga gtt cgt   319
Arg Lys Lys Phe Arg Glu Thr Arg His Pro Ile Tyr Arg Gly Val Arg
            40                  45                  50
caa aga aac tcc ggt aag tgg gtt tct gaa gtg aga gag cca aac aag   367
Gln Arg Asn Ser Gly Lys Trp Val Ser Glu Val Arg Glu Pro Asn Lys
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aaa acc agg att tgg ctc ggg act ttc caa acc gct gag atg gca gct   415
Lys Thr Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala Glu Met Ala Ala
    70                  75                  80
cgt gct cac gac gtc gct gca tta gcc ctc cgt ggc cga tca gca tgt   463
Arg Ala His Asp Val Ala Ala Leu Ala Leu Arg Gly Arg Ser Ala Cys
 85                  90                  95                 100
ctc aac ttc gct gac tcg gct tgg cgg cta cga atc ccg gag tca aca   511
Leu Asn Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile Pro Glu Ser Thr
                105                 110                 115
tgc gcc aag gat atc caa aaa gcg gct gct gaa gcg gcg ttg gct ttt   559
Cys Ala Lys Asp Ile Gln Lys Ala Ala Ala Glu Ala Ala Leu Ala Phe
            120                 125                 130
caa gat gag acg tgt gat acg acg acc acg aat cat ggc ctg gac atg   607
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    150                 155                 160
gcg ttt tat atg gat gag gag aca atg ttt ggg atg ccg act ttg ttg   703
Ala Phe Tyr Met Asp Glu Glu Thr Met Phe Gly Met Pro Thr Leu Leu
165                 170                 175                 180
gat aat atg gct gaa ggc atg ctt tta ccg ccg ccg tct gtt caa tgg   751
Asp Asn Met Ala Glu Gly Met Leu Leu Pro Pro Pro Ser Val Gln Trp
                185                 190                 195
aat cat aat tat gac ggc gaa gga gat ggt gac gtg tcg ctt tgg agt   799
Asn His Asn Tyr Asp Gly Glu Gly Asp Gly Asp Val Ser Leu Trp Ser
            200                 205                 210
tac taatattcga tagtcgtttc catttttgta ctatagtttg aaaatattct        852
Tyr
agttcctttt tttagaatgg ttccttcatt ttattttatt ttattgttgt agaaacgagt 912
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         35                  40                  45
Arg Gly Val Arg Gln Arg Asn Ser Gly Lys Trp Val Ser Glu Val Arg
     50                  55                  60
Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala
 65                  70                  75                  80
Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala Leu Arg Gly
                 85                  90                  95
Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile
            100                 105                 110
Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala Ala Glu Ala
        115                 120                 125
Ala Leu Ala Phe Gln Asp Glu Thr Cys Asp Thr Thr Thr Thr Asn His
    130                 135                 140
Gly Leu Asp Met Glu Glu Thr Met Val Glu Ala Ile Tyr Thr Pro Glu
145                 150                 155                 160
Gln Ser Glu Gly Ala Phe Tyr Met Asp Glu Glu Thr Met Phe Gly Met
                165                 170                 175
Pro Thr Leu Leu Asp Asn Met Ala Glu Gly Met Leu Leu Pro Pro Pro
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tactcttctg atca atg aac tca ttt tct gcc ttt tct gaa atg ttt ggc   170
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                 1               5                  10
tcc gat tac gag tct ccg gtt tcc tca ggc ggt gat tac agt ccg aag   218
Ser Asp Tyr Glu Ser Pro Val Ser Ser Gly Gly Asp Tyr Ser Pro Lys
        15                  20                  25
ctt gcc acg agc tgc ccc aag aaa cca gcg gga agg aag aag ttt cgt   266
Leu Ala Thr Ser Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg
    30                  35                  40
gag act cgt cac cca att tac aga gga gtt cgt caa aga aac tcc ggt   314
Glu Thr Arg His Pro Ile Tyr Arg Gly Val Arg Gln Arg Asn Ser Gly
45                  50                  55                  60
aag tgg gtg tgt gag ttg aga gag cca aac aag aaa acg agg att tgg   362
Lys Trp Val Cys Glu Leu Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp
                65                  70                  75
ctc ggg act ttc caa acc gct gag atg gca gct cgt gct cac gac gtc   410
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            80                  85                  90
gcc gcc ata gct ctc cgt ggc aga tct gcc tgt ctc aat ttc gct gac   458
Ala Ala Ile Ala Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp
        95                  100                 105
tcg gct tgg cgg cta cga atc ccg gaa tca acc tgt gcc aag gaa atc   506
Ser Ala Trp Arg Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Glu Ile
    110                 115                 120
caa aag gcg gcg gct gaa gcc gcg ttg aat ttt caa gat gag atg tgt   554
Gln Lys Ala Ala Ala Glu Ala Ala Leu Asn Phe Gln Asp Glu Met Cys
125                 130                 135                 140
cat atg acg acg gat gct cat ggt ctt gac atg gag gag acc ttg gtg   602
His Met Thr Thr Asp Ala His Gly Leu Asp Met Glu Glu Thr Leu Val
                145                 150                 155
gag gct att tat acg ccg gaa cag agc caa gat gcg ttt tat atg gat   650
Glu Ala Ile Tyr Thr Pro Glu Gln Ser Gln Asp Ala Phe Tyr Met Asp
            160                 165                 170
gaa gag gcg atg ttg ggg atg tct agt ttg ttg gat aac atg gcc gaa   698
Glu Glu Ala Met Leu Gly Met Ser Ser Leu Leu Asp Asn Met Ala Glu
        175                 180                 185
ggg atg ctt tta ccg tcg ccg tcg gtt caa tgg aac tat aat ttt gat   746
Gly Met Leu Leu Pro Ser Pro Ser Val Gln Trp Asn Tyr Asn Phe Asp
    190                 195                 200
gtc gag gga gat gat gac gtg tcc tta tgg agc tat taaaattcga        792
Val Glu Gly Asp Asp Asp Val Ser Leu Trp Ser Tyr
205                 210                 215
tttttatttc catttttggt attatagctt tttatacatt tgatcctttt ttagaatgga 852
tcttcttctt tttttggttg tgagaaacga atgtaaatgg taaaagttgt tgtcaaatgc 912
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         35                  40                  45
Pro Ile Tyr Arg Gly Val Arg Gln Arg Asn Ser Gly Lys Trp Val Cys
     50                  55                  60
Glu Leu Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe
 65                  70                  75                  80
Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Ile Ala
                 85                  90                  95
Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg
            100                 105                 110
Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Glu Ile Gln Lys Ala Ala
        115                 120                 125
Ala Glu Ala Ala Leu Asn Phe Gln Asp Glu Met Cys His Met Thr Thr
    130                 135                 140
Asp Ala His Gly Leu Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr
145                 150                 155                 160
Thr Pro Glu Gln Ser Gln Asp Ala Phe Tyr Met Asp Glu Glu Ala Met
                165                 170                 175
Leu Gly Met Ser Ser Leu Leu Asp Asn Met Ala Glu Gly Met Leu Leu
            180                 185                 190
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        195                 200                 205
Asp Asp Val Ser Leu Trp Ser Tyr
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cgactctaat cctggagtta tcattcacga tagattctta gattgcgact ataaagaaga 180
ag atg gct gta tat gaa caa acc gga acc gag cag ccg aag aaa agg    227
   Met Ala Val Tyr Glu Gln Thr Gly Thr Glu Gln Pro Lys Lys Arg
     1               5                  10                  15
aaa tct agg gct cga gca ggt ggt tta acg gtg gct gat agg cta aag   275
Lys Ser Arg Ala Arg Ala Gly Gly Leu Thr Val Ala Asp Arg Leu Lys
                 20                  25                  30
aag tgg aaa gag tac aac gag att gtt gaa gct tcg gct gtt aaa gaa   323
Lys Trp Lys Glu Tyr Asn Glu Ile Val Glu Ala Ser Ala Val Lys Glu
             35                  40                  45
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Gly Glu Lys Pro Lys Arg Lys Val Pro Ala Lys Gly Ser Lys Lys Gly
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         50                  55                  60
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Cys Met Lys Gly Lys Gly Gly Pro Asp Asn Ser His Cys Ser Phe Arg
     65                  70                  75
gga gtt aga caa agg att tgg ggt aaa tgg gtt gca gag att cga gaa   467
Gly Val Arg Gln Arg Ile Trp Gly Lys Trp Val Ala Glu Ile Arg Glu
 80                  85                  90                  95
ccg aaa ata gga act aga ctt tgg ctt ggt act ttt cct acc gcg gaa   515
Pro Lys Ile Gly Thr Arg Leu Trp Leu Gly Thr Phe Pro Thr Ala Glu
                100                 105                 110
aaa gct gct tcc gct tat gat gaa gcg gct acc gct atg tac ggt tca   563
Lys Ala Ala Ser Ala Tyr Asp Glu Ala Ala Thr Ala Met Tyr Gly Ser
            115                 120                 125
ttg gct cgt ctt aac ttc cct cag tct gtt ggg tct gag ttt act agt   611
Leu Ala Arg Leu Asn Phe Pro Gln Ser Val Gly Ser Glu Phe Thr Ser
        130                 135                 140
acg tct agt caa tct gag gtg tgt acg gtt gaa aat aag gcg gtt gtt   659
Thr Ser Ser Gln Ser Glu Val Cys Thr Val Glu Asn Lys Ala Val Val
    145                 150                 155
tgt ggt gat gtt tgt gtg aag cat gaa gat act gat tgt gaa tct aat   707
Cys Gly Asp Val Cys Val Lys His Glu Asp Thr Asp Cys Glu Ser Asn
160                 165                 170                 175
cca ttt agt cag att tta gat gtt aga gaa gag tct tgt gga acc agg   755
Pro Phe Ser Gln Ile Leu Asp Val Arg Glu Glu Ser Cys Gly Thr Arg
                180                 185                 190
ccg gac agt tgc acg gtt gga cat caa gat atg aat tct tcg ctg aat   803
Pro Asp Ser Cys Thr Val Gly His Gln Asp Met Asn Ser Ser Leu Asn

            195                 200                 205
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Tyr Asp Leu Leu Leu Glu Phe Glu Gln Gln Tyr Trp Gly Gln Val Leu
        210                 215                 220
cag gag aaa gag aaa ccg aag cag gaa gaa gag gag ata cag caa cag   899
Gln Glu Lys Glu Lys Pro Lys Gln Glu Glu Glu Glu Ile Gln Gln Gln
    225                 230                 235
caa cag gaa cag caa cag caa cag ctg caa ccg gat ttg ctt act gtt   947
Gln Gln Glu Gln Gln Gln Gln Gln Leu Gln Pro Asp Leu Leu Thr Val
240                 245                 250                 255
gca gat tac ggt tgg cct tgg tct aat gat att gta aat gat cag act   995
Ala Asp Tyr Gly Trp Pro Trp Ser Asn Asp Ile Val Asn Asp Gln Thr

                260                 265                 270
tct tgg gat cct aat gag tgc ttt gat att aat gaa ctc ctt gga gat   1043
Ser Trp Asp Pro Asn Glu Cys Phe Asp Ile Asn Glu Leu Leu Gly Asp
            275                 280                 285
ttg aat gaa cct ggt ccc cat cag agc caa gac caa aac cac gta aat   1091
Leu Asn Glu Pro Gly Pro His Gln Ser Gln Asp Gln Asn His Val Asn
        290                 295                 300
tct ggt agt tat gat ttg cat ccg ctt cat ctc gag cca cac gat ggt   1139
Ser Gly Ser Tyr Asp Leu His Pro Leu His Leu Glu Pro His Asp Gly
    305                 310                 315
cac gag ttc aat ggt ttg agt tct ctg gat att tgagagttct gaggcaatgg 1192
His Glu Phe Asn Gly Leu Ser Ser Leu Asp Ile
320                 325                 330
tcctacaaga ctacaacata atctttggat tgatcatagg agaaacaaga aataggtgtt 1252
aatgatctga ttcacaatga aaaaatattt aataactcta tagtttttgt tctttccttg 1312
gatcatgaac tgttgcttct catctattga gttaatatag cgaatagcag agtttctctc 1372
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tttcttctct ttgtagaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaayh sakmabgcar 1432
srcsdvsnaa nntrnatnar sarchcntrr agrctrascn csrcaswash tskbabarak 1492
aantamaysa kmasrngnga c 1513

<210> 10
<211> 330
<212> PRT
<213> Arabidopsis thaliana

<400> 10
Met Ala Val Tyr Glu Gln Thr Gly Thr Glu Gln Pro Lys Lys Arg Lys
1 5 10 15
Ser Arg Ala Arg Ala Gly Gly Leu Thr Val Ala Asp Arg Leu Lys Lys
20 25 30
Trp Lys Glu Tyr Asn Glu Ile Val Glu Ala Ser Ala Val Lys Glu Gly
35 40 45
Glu Lys Pro Lys Arg Lys Val Pro Ala Lys Gly Ser Lys Lys Gly Cys
50 55 60
Met Lys Gly Lys Gly Gly Pro Asp Asn Ser His Cys Ser Phe Arg Gly
65 70 75 80
Val Arg Gln Arg Ile Trp Gly Lys Trp Val Ala Glu Ile Arg Glu Pro
85 90 95
Lys Ile Gly Thr Arg Leu Trp Leu Gly Thr Phe Pro Thr Ala Glu Lys
100 105 110
Ala Ala Ser Ala Tyr Asp Glu Ala Ala Thr Ala Met Tyr Gly Ser Leu
115 120 125
Ala Arg Leu Asn Phe Pro Gln Ser Val Gly Ser Glu Phe Thr Ser Thr
130 135 140
Ser Ser Gln Ser Glu Val Cys Thr Val Glu Asn Lys Ala Val Val Cys
145 150 155 160
Gly Asp Val Cys Val Lys His Glu Asp Thr Asp Cys Glu Ser Asn Pro
165 170 175
Phe Ser Gln Ile Leu Asp Val Arg Glu Glu Ser Cys Gly Thr Arg Pro
180 185 190
Asp Ser Cys Thr Val Gly His Gln Asp Met Asn Ser Ser Leu Asn Tyr
195 200 205
Asp Leu Leu Leu Glu Phe Glu Gln Gln Tyr Trp Gly Gln Val Leu Gln
210 215 220
Glu Lys Glu Lys Pro Lys Gln Glu Glu Glu Glu Ile Gln Gln Gln Gln
225 230 235 240
Gln Glu Gln Gln Gln Gln Gln Leu Gln Pro Asp Leu Leu Thr Val Ala
245 250 255
Asp Tyr Gly Trp Pro Trp Ser Asn Asp Ile Val Asn Asp Gln Thr Ser
260 265 270
Trp Asp Pro Asn Glu Cys Phe Asp Ile Asn Glu Leu Leu Gly Asp Leu
275 280 285
Asn Glu Pro Gly Pro His Gln Ser Gln Asp Gln Asn His Val Asn Ser
290 295 300
Gly Ser Tyr Asp Leu His Pro Leu His Leu Glu Pro His Asp Gly His
305 310 315 320
Glu Phe Asn Gly Leu Ser Ser Leu Asp Ile
325 330

<210> 11
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide based on the promoter region of rd29A gene and having HindIII site.

<400> 11
aagcttaagc ttacatcagt ttgaaagaaa 30

<210> 12
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide based on the promoter region of rd29A gene and having HindIII site.

<400> 12
aagcttaagc ttgctttttg gaactcatgt c 31

<210> 13
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide based on DREB1A gene and having BamHI site.

<400> 13
aagcttaagc ttgccataga tgcaattcaa tc 32
<210> 14
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide based on DREB1A gene and having BamHI site.

<400> 14
aagcttaagc ttttccaaag attttttttct ttccaa 36

<210> 15
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide based on the promoter region of rd29A gene and having HindIII site.

<400> 15
ggatccggat ccatgaactc attttctgct 30

<210> 16

<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide based on the promoter region of rd29A gene and having HindIII site.

<400> 16
ggatccggat ccttaataac tccataacga ta 32

<210> 17
<211> 941
<212> DNA
<213> Arabidopsis thaliana
<400> 17
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aaagtttgaa agaaaattta tttcttcgac tcaaaacaaa cttacgaaat ttaggtagaa 120
cttatataca ttatattgta atttttgta acaaaatgtt tttattatta ttatagaatt 180
ttactggtta aattaaaaat gaatagaaaa ggtgaattaa gaggagagag gaggtaaaca 240
ttttcttcta ttttttcata ttttcaggat aaattattgt aaaagtttac aagatttcca 300
tttgactagt gtaaatgagg aatattctct agtaagatca ttatttcatc tacttctttt 360
atcttctacc agtagaggaa taaacaatat ttagctcctt tgtaaataca aattaatttt 420
ccttcttgac atcattcaat tttaatttta cgtataaaat aaaagatcat acctattaga 480
acgattaagg agaaatacaa ttcgaatgag aaggatgtgc cgtttgttat aataaacagc 540
cacacgacgt aaacgtaaaa tgaccacatg atgggccaat agacatggac cgactactaa 600
taatagtaag ttacatttta ggatggaata aatatcatac cgacatcagt tttgaaagaa 660
aagggaaaaa aagaaaaaat aaataaaaga tatactaccg acatgagttc caaaaagcaa 720
aaaaaaagat caagccgaca cagacacgcg tagagagcaa aatgactttg acgtcacacc 780
acgaaaacag acgcttcata cgtgtccctt tatctctctc agtctctcta taaacttagt 840
gagaccctcc tctgttttac tcacaaatat gcaaactaga aaacaatcat caggaataaa 900
gggtttgatt acttctattg gaaagaaaaa aatctttgga a 941

<210> 18
<211> 71
<212> DNA
<213> Arabidopsis thaliana

<400> 18
cagtttgaaa gaaaagggaa aaaaagaaaa aataaataaa agatatacta ccgacatgag 60
ttccaaaaag c 71

<210> 19
<211> 71
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide having a partially mutated sequence within the DRE region.

<400> 19
cagtttgaaa gaaaagggaa aaaaagaaaa aataaataaa agatatattt tcgacatgag 60
ttccaaaaag c 71

<210> 20
<211> 71

<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide having a partially mutated sequence within the DRE region.

<400> 20
cagtttgaaa gaaaagggaa aaaaagaaaa aataaataaa agatatacta cttttatgag 60
ttccaaaaag c 71

<210> 21
<211> 71
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide having a partially mutated sequence within the DRE region.

<400> 21
cagtttgaaa gaaaagggaa aaaaagaaaa aataaataaa agatatacta ccgacaaaag 60
ttccaaaaag c 71

<210> 22
<211> 71
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide having a partially mutated sequence outside the DRE region.

<400> 22
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caacaaaaag c 71

<210> 23
<211> 71
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide having a partially mutated sequence outside the DRE region.

<400> 23
cagtttgaaa gaaaagggaa aaaaagaaaa aataaataaa agatatacta ccgacatgag 60
ttcggttaag c 71